

AMENDMENT

In the Claims:

Please cancel claims 33-67 as drawn to non-elected inventions.

RESPONSE

I. Restriction Requirement

The Examiner has determined that the original claims are directed to ten separate and distinct inventions under 35 U.S.C. § 121, as follows:

- Group I: Claims 1-32, said to be drawn to DNA, host cells and expression vectors, classified in class 536, subclass 23.1.
- Group II: Claims 36-39, 41, said to be drawn to protein compositions and antibodies, classified in class 530, subclass 350.
- Group III: Claim 40, said to be drawn to an enzyme subunit, classified in class 530, subclass 300.
- Group IV: Claims 33, 34, said to be drawn to methods of detecting DNA in a sample, classified in class 435, subclass 6.
- Group V: Claim 35, said to be drawn to methods of expressing DNA, classified in class 435, subclass 69.1.
- Group VI: Claim 42, said to be drawn to methods of identifying a gene, classified in class 435, subclass 69.3.
- Group VII: Claims 43-47, said to be drawn to methods for identifying a transcriptional inhibitor, classified in class 435, subclass 69.2.
- Group VIII: Claim 48, said to be drawn to methods for identifying Tat protein, classified in class 435, subclass 7.1.
- Group IX: Claims 49-58, said to be drawn to methods of identifying viral transcription inhibitor, classified in class 935, subclass 76.
- Group X: Claims 59-67, said to be drawn to other methods of identifying a viral transcription inhibitor, classified in class 935, subclass 77.

II. Response to Restriction Requirement

Applicant hereby elects the Group I invention (claims 1-32) without traverse. Accordingly, claims 33-67 are canceled as drawn to non-elected inventions. Applicant reserves the right to refile claims to the non-elected inventions in one or more future applications retaining the priority date of the present case and the earlier cited priority applications.

III. Species Election

The Requirement further indicates that the Group I invention contains claims directed to the following patentably distinct species:

Species (a): Full length DNA and corresponding SEQ ID NO; and

Species (b): Full length DNA and full length kinase subunit and corresponding SEQ ID NO.

Additionally, should species (b) be elected, the Requirement requests election of one sub-species as follows:

Sub-species 1): a single species vector; and

Sub-species 2): two distinct expression vectors.

Species (a) therefore encompasses DNA segments comprising the full length kinase or the full length large subunit; and species (b) encompasses DNA segments comprising the full length kinase and the full length large subunit. This is consistent with the sub-species set forth for species (b), and the Examiner's statement that no claims are generic to species (a) and species (b).

IV. Response to Species Election Requirement

Applicant elects, without traverse, species (a) to begin examination on the merits. In light of the present species election, Applicant believes that at least claims 1-22 and 27-30 read on the elected species.

Claims 23-26, 31 and 32 are also pending in the case, and are available for rejoinder in this application as provided by 37 C.F.R. § 1.141.

V. Status of the Claims

Claims 33-67, representing the Group II-X inventions, respectively, have been canceled without prejudice or disclaimer as drawn to non-elected inventions.

No claims within the Group I invention have been amended. No claims within the Group I invention have been canceled. No new claims have been added.

Claims 1-32 are presently pending in the case. For the convenience of the Examiner, a copy of the pending claims is attached hereto as **Exhibit A**.

VI. Conclusion

The present document is a complete response to the Restriction and Species Election Requirement. Should Examiner Smith have any questions or comments, or believe that certain amendments to the claims might serve to even further improve their clarity, a telephone call to the undersigned Applicant's representative is earnestly solicited.

Respectfully submitted,

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EXHIBIT A

EXHIBIT A
PENDING CLAIMS IN U.S. SERIAL NO. 08/951,188 (Att. Dkt. IOWA:012)

1. A DNA segment comprising an isolated coding region that encodes a substantially full length P-TEFb subunit, wherein the coding region is characterized as:
 - (a) encoding a substantially full length P-TEFb kinase subunit having the amino acid sequence of SEQ ID NO:2; or
 - (b) encoding a substantially full length P-TEFb large subunit that includes a contiguous sequence of at least about 7 amino acids from SEQ ID NO:4, SEQ ID NO:45, SEQ ID NO:47 or SEQ ID NO:50; or as a substantially full length coding region that hybridizes to the nucleotide sequence of SEQ ID NO:3, SEQ ID NO:43 or SEQ ID NO:48 under stringent hybridization conditions.
2. The DNA segment of claim 1, wherein said isolated coding region encodes a substantially full length P-TEFb kinase subunit having the amino acid sequence of SEQ ID NO:2.
3. The DNA segment of claim 1, wherein said isolated coding region has the nucleotide sequence from position 115 to position 1327 of SEQ ID NO:1.
4. The DNA segment of claim 1, wherein said isolated coding region encodes a substantially full length P-TEFb large subunit that includes a contiguous sequence of at least about 7 amino acids from SEQ ID NO:4, SEQ ID NO:45, SEQ ID NO:47 or SEQ ID NO:50; or as a substantially full length coding region that hybridizes to the nucleotide sequence of SEQ ID NO:3, SEQ ID NO:43 or SEQ ID NO:48 under stringent hybridization conditions.
5. The DNA segment of claim 1, wherein said isolated coding region encodes a substantially full length P-TEFb large subunit that includes a contiguous sequence of at least about 7 amino acids from SEQ ID NO:4, SEQ ID NO:45, SEQ ID NO:47 or SEQ ID NO:50 and wherein said coding region hybridizes to the nucleotide sequence of SEQ ID NO:3, SEQ ID NO:43 or SEQ ID NO:48 under stringent hybridization conditions.
6. The DNA segment of claim 4, wherein said isolated coding region encodes a substantially full length P-TEFb large subunit that includes a contiguous sequence of at least about 7 amino acids from SEQ ID NO:4, SEQ ID NO:45, SEQ ID NO:47 or SEQ ID NO:50.

7. The DNA segment of claim 6, wherein said isolated coding region encodes a P-TEFb large subunit having the amino acid sequence of SEQ ID NO:4, SEQ ID NO:45, SEQ ID NO:47 or SEQ ID NO:50.
8. The DNA segment of claim 7, wherein said isolated coding region encodes a P-TEFb large subunit having the amino acid sequence of SEQ ID NO:45.
9. The DNA segment of claim 7, wherein said isolated coding region encodes a P-TEFb large subunit having the amino acid sequence of SEQ ID NO:47.
10. The DNA segment of claim 7, wherein said isolated coding region encodes a P-TEFb large subunit having the amino acid sequence of SEQ ID NO:50.
11. The DNA segment of claim 4, wherein said isolated coding region is a substantially full length coding region that hybridizes to the nucleotide sequence of SEQ ID NO:3, SEQ ID NO:43 or SEQ ID NO:48 under stringent hybridization conditions.
12. The DNA segment of claim 11, wherein said isolated coding region has the nucleotide sequence of SEQ ID NO:44.
13. The DNA segment of claim 11, wherein said isolated coding region has the nucleotide sequence of SEQ ID NO:46.
14. The DNA segment of claim 11, wherein said isolated coding region has the nucleotide sequence of SEQ ID NO:49.
15. The DNA segment of claim 1, wherein said DNA segment comprises a first coding region that encodes a substantially full length P-TEFb kinase subunit and a second coding region that encodes a substantially full length P-TEFb large subunit.
16. The DNA segment of claim 15, wherein said second coding region encodes a P-TEFb large subunit that has the amino acid sequence of SEQ ID NO:45, SEQ ID NO:47 or SEQ ID NO:50.

17. The DNA segment of claim 16, wherein said first coding region encodes a P-TEFb kinase subunit that has the amino acid sequence of SEQ ID NO:6.
18. The DNA segment of claim 16, wherein said second coding region has the nucleotide sequence of SEQ ID NO:44, SEQ ID NO:46 or SEQ ID NO:49, and wherein said first coding region has the nucleotide sequence of SEQ ID NO:5.
19. The DNA segment of claim 1, wherein said isolated coding region is operatively attached to a second coding region that encodes a selected peptide or protein sequence, said DNA segment encoding a P-TEFb subunit fusion protein.
20. The DNA segment of claim 1, operatively positioned under the control of a promoter.
21. The DNA segment of claim 20, further defined as a recombinant vector.
22. The DNA segment of claim 20, comprised within a recombinant host cell.
23. An expression system comprising:
 - (a) a first expression unit comprising, under the transcriptional control of a promoter, a first coding region that encodes a substantially full length P-TEFb kinase subunit that includes a contiguous sequence of at least about 7 amino acids from SEQ ID NO:2 or SEQ ID NO:6; and
 - (b) a second expression unit comprising, under the transcriptional control of a promoter, a second coding region that encodes a substantially full length P-TEFb large subunit that includes a contiguous sequence of at least about 7 amino acids from SEQ ID NO:4, SEQ ID NO:45, SEQ ID NO:47 or SEQ ID NO:50.
24. The expression system of claim 23, wherein said first and said second expression units are comprised on a single expression vector.
25. The expression system of claim 23, wherein said first and said second expression units are comprised on two distinct expression vectors.

26. The expression system of claim 23, wherein said expression system is comprised within a recombinant host cell.
27. A recombinant host cell comprising at least a first DNA segment in accordance with claim 1.
28. The recombinant host cell of claim 27, wherein said cell is a prokaryotic host cell.
29. The recombinant host cell of claim 27, wherein said cell is a eukaryotic host cell.
30. The recombinant host cell of claim 27, wherein said cell further comprises an HIV Tat protein.
31. The recombinant host cell of claim 27, wherein said cell comprises a first DNA segment that encodes a substantially full length P-TEFb kinase subunit and a second DNA segment that encodes a substantially full length P-TEFb large subunit.
32. The recombinant host cell of claim 31, wherein said first and second DNA segments are comprised within a single expression vector.